

| Sequences producing significant alignments: | | | Score (bits) | E Value |
|---|-------------------------------------|-----|-----------------|------------|
| gi 55642389 ref XP_523094.1 | PREDICTED: similar to Presenil... | 452 | e-126 | |
| gi 37182518 gb AAQ89061.1 | TAAV688 [Homo sapiens] | 451 | e-125 | G |
| gi 50726954 ref NP_112591.2 | presenilin stabilization facto... | 449 | e-125 | G |
| gi 12052866 emb CAB66606.1 | hypothetical protein [Homo sapi... | 447 | e-124 | G |
| gi 55726744 emb CAH90134.1 | hypothetical protein [Pongo pyg... | 444 | e-123 | |
| gi 29243936 ref NP_808251.1 | hypothetical protein 4632417K0... | 391 | e-107 | G |
| gi 34864291 ref XP_217185.2 | similar to RIKEN cDNA 0610008A... | 377 | e-103 | G |
| gi 21492616 ref NP_080950.1 | RIKEN cDNA 0610008A10 [Mus mus... | 369 | e-101 | G |
| gi 37682171 gb AAQ98012.1 | anterior pharynx defective 1B-li... | 284 | 2e-75 | G |
| gi 34864287 ref XP_343418.1 | similar to RIKEN cDNA 0610008A... | 282 | 7e-75 | G |
| gi 17389295 gb AAH17699.1 | APH-1A protein [Homo sapiens] >g... | 256 | 7e-67 | G |
| gi 15990414 gb AAH15568.1 | APH-1A protein [Homo sapiens] >g... | 254 | 2e-66 | G |
| gi 12654775 gb AAH01230.1 | APH-1A protein [Homo sapiens] | 254 | 2e-66 | G |
| gi 56268871 gb AAH87081.1 | Unknown (protein for MGC:94545) ... | 253 | 5e-66 | |
| gi 22203751 ref NP_666216.1 | anterior pharynx defective 1A ... | 252 | 8e-66 | G |
| gi 34858248 ref XP_345252.1 | similar to Aph1a-pending prote... | 252 | 1e-65 | G |
| gi 18848275 gb AAH24111.1 | 6530402N02Rik protein [Mus muscu... | 251 | 2e-65 | G |

| | | | | |
|-----------------------------|---|-----|-------|---|
| gi 7705787 ref NP_057106.1 | CGI-78 protein [Homo sapiens] >... | 248 | 2e-64 | G |
| gi 26324468 dbj BAC25988.1 | unnamed protein product [Mus mu... | 246 | 6e-64 | G |
| gi 47214485 emb CAG12490.1 | unnamed protein product [Tetrao... | 211 | 3e-53 | |
| gi 48095709 ref XP_392345.1 | similar to CG2855-PA [Apis mel... | 178 | 1e-43 | G |
| gi 54644318 gb EAL33059.1 | GA15487-PA [Drosophila pseudoobs... | 172 | 1e-41 | |
| gi 20129183 ref NP_608710.1 | CG2855-PA [Drosophila melanoga... | 164 | 3e-39 | G |
| gi 55236032 gb EAA14158.3 | ENSANGP00000015809 [Anopheles ga... | 164 | 4e-39 | |
| gi 26347159 dbj BAC37228.1 | unnamed protein product [Mus mu... | 162 | 1e-38 | G |
| gi 31233667 ref XP_318923.1 | ENSANGP00000015809 [Anopheles ... | 158 | 2e-37 | G |
| gi 50806123 ref XP_428797.1 | PREDICTED: similar to Anterior... | 154 | 3e-36 | G |
| gi 56204871 emb CAI22813.1 | likely ortholog of C. elegans a... | 145 | 1e-33 | |
| gi 50809568 ref XP_429030.1 | PREDICTED: similar to anterior... | 121 | 3e-26 | G |
| gi 39580694 emb CAE70374.1 | Hypothetical protein CBG16933 [... | 81 | 4e-14 | |
| gi 17509423 ref NP_492469.1 | i-78 protein like, Anterior PH... | 74 | 7e-12 | G |
| gi 50252282 dbj BAD28287.1 | presenilin stabilization factor... | 71 | 3e-11 | |
| gi 20453379 gb AAM19928.1 | At2g31440/T28P16.7 [Arabidopsis ... | 70 | 6e-11 | G |
| gi 21594204 gb AAM65980.1 | unknown [Arabidopsis thaliana] | 69 | 1e-10 | |
| gi 56500904 emb CAH94855.1 | conserved hypothetical protein ... | 37 | 0.90 | |
| gi 22024126 ref NP_610786.2 | CG8545-PA [Drosophila melanoga... | 36 | 1.5 | G |
| gi 32403290 ref XP_322258.1 | hypothetical protein [Neurospo... | 35 | 2.0 | G |
| gi 9837379 gb AAG00551.1 | retinitis pigmentosa GTPase regul... | 35 | 2.0 | |
| gi 31621286 tpg DAA01153.1 | TPA: RT11 [Mus musculus] >gi 46... | 35 | 2.6 | G |
| gi 2209198 gb AAB61441.1 | LOX6 [Helobdella robusta] | 35 | 2.6 | |
| gi 32414609 ref XP_327784.1 | hypothetical protein [Neurospo... | 35 | 3.4 | G |
| gi 55588200 ref XP_513809.1 | PREDICTED: hypothetical protei... | 35 | 3.4 | |
| gi 51458782 ref XP_371313.2 | PREDICTED: similar to dJ14N1.2... | 35 | 3.4 | G |
| gi 12314268 emb CAC13173.1 | novel S-100\ICaBP type calcium... | 35 | 3.4 | |
| gi 32423411 ref XP_332143.1 | predicted protein [Neurospora ... | 34 | 4.5 | G |
| gi 53719504 ref YP_108490.1 | putative lipoprotein [Burkhold... | 34 | 4.5 | G |
| gi 53723509 ref YP_102951.1 | TPR domain protein [Burkholder... | 34 | 4.5 | G |
| gi 42554029 gb EAA76872.1 | hypothetical protein FG07524.1 [... | 34 | 5.8 | G |
| gi 46444603 gb EAL03877.1 | hypothetical protein CaO19.1574 ... | 34 | 5.8 | |
| gi 46444453 gb EAL03728.1 | hypothetical protein CaO19.9147 ... | 34 | 5.8 | |
| gi 56315671 emb CAI10315.1 | hypothetical protein [Azoarcus ... | 34 | 5.8 | |
| gi 46228566 gb EAK89436.1 | hypothetical protein with possib... | 34 | 5.8 | |
| gi 7488765 pir T10863 | extensin precursor - kidney bean >gi... | 23 | 7.0 | |
| gi 41054255 ref NP_956076.1 | nuclear autoantigenic sperm pr... | 33 | 7.6 | G |
| gi 51557560 ref YP_068394.1 | putative ORF-3 protein [Suid h... | 33 | 7.6 | G |
| gi 22328344 ref NP_680595.1 | hypothetical protein [Arabidop... | 33 | 7.6 | G |
| gi 32563629 ref NP_491994.2 | chromo domain and SNF2 related... | 33 | 9.9 | G |
| gi 23508533 ref NP_701202.1 | hypothetical protein [Plasmodi... | 33 | 9.9 | G |
| gi 55741482 ref NP_055840.1 | myelin transcription factor 1-... | 33 | 9.9 | G |
| gi 51708299 ref XP_143396.3 | PREDICTED: similar to dJ14N1.2... | 33 | 9.9 | G |
| gi 50418016 gb AAH77951.1 | Irx2-A protein [Xenopus laevis] | 33 | 9.9 | G |
| gi 7504867 pir T23056 | hypothetical protein H06001.2 - Caen... | 33 | 9.9 | |
| gi 9837383 gb AAG00553.1 | retinitis pigmentosa GTPase regul... | 33 | 9.9 | |

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|55642389|ref|XP_523094.1| PREDICTED: similar to Presenilin stabilization fac
troglodytes]
Length = 389

Score = 452 bits (1162), Expect = e-126
Identities = 231/259 (89%), Positives = 231/259 (89%)
Frame = +3

Query: 3 VAMTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARV 182
VAMTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARV
Sbjct: 131 VAMTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARV 190

Query: 183 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 362
IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY
Sbjct: 191 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 250

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFF 542
VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFF
Sbjct: 251 VSGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFF 310

Query: 543 DGCEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 722
DGCEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL
Sbjct: 311 DGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSL 370

Query: 723 KLCLLCQDKNFLLYNQRSR 779
KLCLLCQDKNFLLYNQRSR
Sbjct: 371 KLCLLCQDKNFLLYNQRSR 389

☐ >gi|37182518|gb|AAQ89061.1| ☒ TAAV688 [Homo sapiens]
Length = 257

Score = 451 bits (1159), Expect = e-125
Identities = 230/257 (89%), Positives = 230/257 (89%)
Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGA MARVII
Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS
Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG 548
GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG
Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
CLLCQDKNFLLYNQRSR
Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|50726954|ref|NP_112591.2| [G] presenilin stabilization factor-like [Homo sapiens]
 gi|18088649|gb|AAH20905.1| [G] Presenilin stabilization factor-like [Homo sapiens]
 Length = 257

Score = 449 bits (1154), Expect = e-125
 Identities = 229/257 (89%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDKNFLLYNQRSR
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|12052866|emb|CAB66606.1| [G] hypothetical protein [Homo sapiens]
 gi|37077447|sp|Q8WW43|AP1B_HUMAN [G] Gamma-secretase subunit APH-1B (APH-1b) (Aph-1
 stabilization factor-like)
 gi|24637564|gb|AAN63817.1| [G] presenilin stabilization factor-like protein [Homo sapiens]
 Length = 257

Score = 447 bits (1150), Expect = e-124
 Identities = 228/257 (88%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DNKDGPTQKYLLIFGAFVSVYI+EMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGAFVSVYIREMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDKNFLLYNQRSR
 Sbjct: 241 CLLCQDKNFLLYNQRSR 257

>gi|55726744|emb|CAH90134.1| hypothetical protein [Pongo pygmaeus]
 Length = 257

Score = 444 bits (1142), Expect = e-123
 Identities = 226/257 (87%), Positives = 228/257 (88%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DNKDGPTQKYLLIFG FVSVYIQEMFRFAYY+LLKKASEGLKSINPGETAPSMRLLAYVS
 Sbjct: 61 DNKDGPTQKYLLIFGTFVSVYIQEMFRFAYYRLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG 548
 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 728
 CEKKKWG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL
 Sbjct: 181 CEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

>gi|29243936|ref|NP_808251.1| [G] hypothetical protein 4632417K02 [Mus musculus]
 gi|50927492|gb|AAH79659.1| [G] Hypothetical protein 4632417K02 [Mus musculus]
 gi|26340556|dbj|BAC33940.1| [G] unnamed protein product [Mus musculus]
 gi|37077156|sp|Q8C7N7|AP1B_MOUSE [G] Gamma-secretase subunit APH-1B
 Length = 257

Score = 391 bits (1004), Expect = e-107
 Identities = 194/257 (75%), Positives = 210/257 (81%)
 Frame = +3



Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGFPALALYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAGFPALALYVFTIATDPLRVIIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYYKLLKKASEGLKSINP ETAPSMRLLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFHWGIVFFDG 548
 GLGFGIMSGVFSFVNTLS+SLGPGTVGIHGDSPQFFL SAFMTLV+I+LHVFHWG+VFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSNSLPGPTVGIHGDSPQFFLNSAFMTLVVIMLHVFHWGVVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKL 728
 CEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSLKL
 Sbjct: 181 CEKNKWYTLTLLTVLLTHLVVSTQTFLLSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRRSR 779
 CLLCQDK+FLLYNQRRSR
 Sbjct: 241 CLLCQDKDFLLYNQRRSR 257

 >gi|34864291|ref|XP_217185.2|  similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]
 Length = 257

Score = 377 bits (968), Expect = e-103
 Identities = 189/257 (73%), Positives = 207/257 (80%)
 Frame = +3






Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXXXXXXMARVII 188
 MTA VFFGCAFIAGFPALALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAPVFFGCAFIAGFPALALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKASEGLKSINP ETAPSMRLLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFVGIVFFDG 548
 GLGFGIMSGVFSFVNTLS++LPGTVGIHGDSPQFFL SAFMTLVII+LHVFVGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSFVNTLSNALPGTVGIHGDSPQFFLNSAFMTLVIIIMLHVFVGIVFFDG 180

Query: 549 CEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKL 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 181 CEKNKWYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFVAGGSRRSLKL 240

Query: 729 CLLCQDKNFLLYNQRRSR 779
 CLLCQDK+FLLYNQRRSR
 Sbjct: 241 CLLCQDKDFLLYNQRRSR 257

 >gi|21492616|ref|NP_080950.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|38648719|gb|AAH63254.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|29747906|gb|AAH50923.1|  RIKEN cDNA 0610008A10 [Mus musculus]
 gi|37077773|sp|Q9DCZ9|AP1C_MOUSE Putative gamma-secretase subunit APH-1C
 gi|12832198|dbj|BAB22004.1|  unnamed protein product [Mus musculus]
 Length = 258

Score = 369 bits (948), Expect = e-101
 Identities = 186/258 (72%), Positives = 204/258 (79%), Gaps = 1/258 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXXXXXXMARVII 188
 MT VFFGCAFIAGFPA ALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTLPVFFGCAFIAGFPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSMFVFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGET-APSMRLLAYV 365
 +N+D Q YLLIFGA +SV IQE+FR AYYKLLKKASEGLKSINP E APSMRLLAYV
 Sbjct: 61 NNRDESQVQNYLLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFFD 545
 SGLGFGIMSGVFSFVNTLS+SLGPCTVGIHGDSPOFFL SAFMTLV+I+LHVFWG+VFFD
 Sbjct: 121 SGLGFGIMSGVFSFVNTLSNSLGPCTVGIHGDSPOFFLNSAFMTLVVIMLHVFWGVVFFD 180

Query: 546 GCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSK 725
 GCEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSK
 Sbjct: 181 GCEKNKWYTLTLTVLLTHLVVSTQTFSPYYEVNLTAYIIMVLMGIWAFYVAGGSCRSK 240

Query: 726 LCLLCQDKNFLLYNQSR 779
 CLLCQDK+FLLYNQSR
 Sbjct: 241 FCLLCQDKDFLLYNQSR 258

>gi|37682171|gb|AAQ98012.1| [G] anterior pharynx defective 1B-like [Danio rerio]
 gi|41056229|ref|NP_956409.1| [G] anterior pharynx defective 1B [Danio rerio]
 gi|22001127|gb|AAM88325.1| [G] Aph-1 protein [Danio rerio]
 gi|47939453|gb|AAH71492.1| [G] Anterior pharynx defective 1B [Danio rerio]
 gi|37077309|sp|Q8JHE9|AP1B_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx
 1b)
 Length = 258

Score = 284 bits (726), Expect = 2e-75
 Identities = 147/259 (56%), Positives = 183/259 (70%), Gaps = 2/259 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAPGALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MT AVFFGC FIAFGPA+AL++FTIA +PLR+IFLIAGA + V I
 Sbjct: 1 MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFLIAGAFFWLVSLLLSSLVWFIT-VQI 59

Query: 189 DNKDGPTQKY-LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAY 362
 NK+ TQ+ LLIFG +SV +QE FR+ YY+LLKKA+EGL +++ +T P SMR LAY
 Sbjct: 60 SNKNSATQQRGLLIFGVVLSVLLQEAFFRYGYRLLKKANEGLLALSQEDTMPISMRQLAY 119

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPOFFLYSAFMTLVIILLHVFVGIVFF 542
 VSGLGFG MSG FS VN LSDSLGPCTVGIHG+S +F+ SAFMTL IILLH+FWG+VFF
 Sbjct: 120 VSGLGFGMSGAFSVVNILSDSLGPCTVGIHGESHYFISSAFMTLAIILLHMFVGIVFF 179

Query: 543 DGCEKKKWGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSK 722
 + CE+++W S TF++ +Y +L +IIL +M WA+L AGGS R+L
 Sbjct: 180 EACERQRWWALGAVVASHLVVSLTFVNPYQGLIPTIYIILSVMAVWAYLCAGGSLRNL 239

Query: 723 KLCLLCQDKNFLLYNQSR 779
 KLCL C+DK+FLL N R R
 Sbjct: 240 KLCLTCKDKDFLLANHRPR 258

>gi|34864287|ref|XP_343418.1| [G] similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]
 Length = 216

Score = 282 bits (722), Expect = 7e-75
 Identities = 151/257 (58%), Positives = 168/257 (65%)
 Frame = +3








Query: 9 MTAAVFFGCAFIAPGALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAPGAL+LYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAPGALSIVFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKA+EGLKSINP ETAPSMRLLAY
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGGLKSINPEETAPSMRLLAY-- 118

Query: 369 GLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFDG 548
 AFMTLVII+LHVFVGIVFFDG
 Sbjct: 119 -----AFMTLVIIIMLHVFVGIVFFDG 139

Query: 549 CEKKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLK 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 140 CEKNKWYILLTVLLTHLLVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKL 199

Query: 729 CLLCQDKNFLLYNQRRSR 779
 CLLCQDK+FLLYNQRRSR
 Sbjct: 200 CLLCQDKDFLLYNQRRSR 216

 >gi|17389295|gb|AAH17699.1|  APH-1A protein [Homo sapiens]
 gi|14250557|gb|AAH08732.1|  APH-1A protein [Homo sapiens]
 gi|14550502|gb|AAH09501.1|  APH-1A protein [Homo sapiens]
 gi|37183020|gb|AAQ89310.1|  GAAV579 [Homo sapiens]
 gi|56204870|emb|CAI22812.1| likely ortholog of C. elegans anterior pharynx defect
 (APH-1A) [Homo sapiens]
 gi|25989508|gb|AAM61955.1|  presenilin stabilization factor a [Homo sapiens]
 gi|22761292|dbj|BAC11529.1|  unnamed protein product [Homo sapiens]
 Length = 247

Score = 256 bits (653), Expect = 7e-67
 Identities = 129/247 (52%), Positives = 166/247 (67%), Gaps = 1/247 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXXXXXXMARVII 188
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +
 Sbjct: 1 MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVWVILVHVT 60

Query: 189 DNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAYV 365
 D D Q LLIFGA VSV +QE+FRFAYYKLLKKA EGL S++ +P S+R +AYV
 Sbjct: 61 DRSDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLPGPTVGIHGDSPQFFLYSAFMTLVIILLHVFVGIVFFD 545
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD
 Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGIVHGDSPYYFLTSAFLTAATILLHTFWGVVFFD 180

Query: 546 GCEKKKKWGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLK 725
 CE++++ S TF++ +Y +L + + V MG WAF+ AGGS RS++
 Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLCQD 746
 LLC+D
 Sbjct: 241 RSLCKD 247

 >gi|15990414|gb|AAH15568.1|  APH-1A protein [Homo sapiens]
 gi|18088501|gb|AAH20590.1|  APH-1A protein [Homo sapiens]